

us-09-963-333-7.rst

at Jul 27 13:16:46 2002

GenCore version 4.5
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nucleic - nucleic search, using sw model

on: July 26, 2002, 15:13:16 ; Search time 3006.25 seconds
(without alignments)
5329.193 Million cell updates/sec

le: US-09-963-333-7
fect score: 1187
uence: 1 gatcgccactgactca.....gaggagggcgctgggga 1187

ring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

ched: 13736207 seqs, 6748477542 residues

al number of hits satisfying chosen parameters: 27472414

inum DB seq length: 0

inum DB seq length: 200000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

abase :

- EST: *
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_estro:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_hic:*
 - 12: gb_gss:*
 - 13: em_gss_hum:*
 - 14: em_gss_inv:*
 - 15: em_gss_pln:*
 - 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

sult No.	Score	Query Match	Length	ID	Description
1	335.8	28.3	1060	BM456638	AGENCOURT
2	329.8	27.8	741	AU118644	AU118644
3	328.2	27.6	739	AU143295	AU143295
4	328.2	27.6	819	AU143180	AU143180
5	327.8	27.6	786	AL545940	AL545940
6	315.8	26.6	985	BM466216	AGENCOURT
7	310.4	26.1	668	AL541351	AL541351
8	303.8	25.6	938	AL551390	AL551390
9	295.8	24.9	738	AU130205	AU130205
10	294.2	24.8	711	AU142980	AU142980
11	288.6	24.3	526	AU128726	AU128726
12	286.8	24.2	529	BE794349	BE794349
13	285	24.1	905	BI597722	BI597722
14	280.2	23.9	935	AL542409	AL542409
15	279.6	23.8	524	BM478045	AGENCOURT
16	278.8	23.8	1045	BM478045	AGENCOURT

18	277	23.3	832	10	BF685317
19	276.8	23.3	742	9	AL548721
20	275.2	22.5	1020	9	AL547612
21	266.6	22.5	664	10	BI520187
22	266	22.4	963	10	EG337540
23	265.8	22.4	809	9	AU117646
24	265.4	22.4	538	10	BI668571
25	265.2	22.3	888	10	BM413631
26	265	22.3	439	10	BF689564
27	263.8	22.2	672	10	EG574267
28	263	22.2	950	9	AL550812
29	262.8	22.1	688	9	AL543217
30	258.8	21.8	836	10	BI822334
31	258.8	21.8	1533	11	BC018858
32	258	21.7	783	10	BE731577
33	255.4	21.5	932	9	AL528821
34	254.8	21.5	442	10	BE280876
35	254.8	21.5	465	10	EG749145
36	253.8	21.4	454	10	BE389795
37	252.2	21.2	761	10	BE409629
38	251.4	21.2	810	10	BE882773
39	248.2	20.9	1035	10	BM473957
40	246.8	20.8	995	9	AL515911
41	245.8	20.7	932	9	AL551817
42	242.8	20.5	893	10	BM457044
43	240.8	20.3	458	10	EG329382
44	240.8	20.3	854	9	AL556369
45	238.8	20.1	897	9	AL519416

ALIGNMENTS

RESULT 1
BM456638
LOCUS
DEFINITION
AGENCOURT_6408748 NIH_MGC_85 Homo sapiens cdna clone IMAGE:5496315
5', mRNA sequence. 1060 bp mRNA linear EST 05-FEB-2002

ACCESSION
BM456638
VERSION
BM456638.1 GI:18505678
KEYWORDS
EST.
SOURCE
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 1060)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS
Contact: Robert Strausberg, Ph.D.

JOURNAL
Contact: cgabps@mail.nih.gov

COMMENT
Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12124 row: k column: 04

High quality sequence stop: 530.

Location/Qualifiers

source

1. 1060

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5496315"

/tissue_type="lymphoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lymph; Vector: pCMV-SPORT6; Site:1: NotI;

Site:2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.867 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

[illegible]

Db 298 CGCGCTACAGCCCTGAGAGATGA 319

Search completed: July 26, 2002, 15:13:23
Job time: 26887 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2002, 17:57:13 ; Search time 406.4 Seconds
(without alignments)
5014.708 Million cell updates/sec

Title: US-09-963-333-7
Perfect score: 1187
Sequence: 1 gatcgccactgcactcca.....gaggaggcgcgctgggga 1187

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %	Score	Match	Length	ID	Description
1	1163.8	98.0	18596	22	AAF31109	Thymidylate synthase
2	1163.8	98.0	18596	22	AAC91215	Human thymidylate
3	287.2	24.2	3298	24	AAS94945	Human DNA sequence
C 4	206.8	17.4	9519	22	AAL37169	Human musculoskele
C 5	206.8	17.4	56632	22	AAK65581	Human immune/haema
C 6	206.4	17.4	9731	22	AAL04943	Human reproductive
C 7	205.8	17.3	1539	23	AAS84960	DNA encoding novel
C 8	204.6	17.2	11453	22	AAK73272	Human immune/haema
C 9	204.6	17.2	11553	22	AAK73271	Human immune/haema

C 10	204.2	17.2	37449	22	AAK66874	Human immune/haema
C 11	204.2	17.2	56743	22	AAK68202	Human immune/haema
C 12	204.2	17.2	56743	22	AAK81760	Human immune/haema
C 13	203.6	17.2	20601	22	AAK79760	Human immune/haema
C 14	202.6	17.1	22916	22	AAK65305	Human immune/haema
C 15	201.8	17.0	10820	22	ABA15598	Human nervous syst
C 16	201.2	17.0	5591	22	ABA15206	Human nervous syst
C 17	201.2	17.0	5591	22	AAK52300	Genomic sequence #
C 18	200	16.8	9060	24	AAK52300	Human genomic DNA
C 19	200	16.8	9060	24	AAK52300	Human genomic DNA
C 20	199.4	16.8	32169	22	ABA14358	Human nervous syst
C 21	198.6	16.7	32173	22	ABA07767	Human ovarian and
C 22	198.6	16.7	32173	22	AAK03558	Human reproductive
C 23	198.6	16.7	38928	22	AAK68452	Human immune/haema
C 24	197.8	16.7	646	22	AAK44995	cDNA encoding nove
C 25	197.6	16.6	7017	22	AAK37408	Human musculoskele
C 26	197.6	16.6	50000	21	AAK96365	Polymorphic repeat
C 27	197.4	16.6	45546	20	AAK23520	Human kidney amino
C 28	196.8	16.6	97662	22	AAK83908	Genomic sequence o
C 29	196.8	16.6	106746	21	AAK10225	Human PCTA-1 genom
C 30	196.6	16.6	7537	22	AAK56235	Human cardiovascular
C 31	196.6	16.6	7537	22	AAK56433	Human immune/haema
C 32	196.6	16.6	10483	22	AAK80686	Human immune/haema
C 33	196.6	16.6	17357	22	AAK86680	Human immune/haema
C 34	196.6	16.6	17363	22	AAK86681	Human immune/haema
C 35	196.6	16.6	325791	22	AAK43104	Human Oestrogen re
C 36	196.4	16.5	13927	22	AAK97853	Human neuroblastom
C 37	196.4	16.5	32012	22	AAK05864	Human reproductive
C 38	196.4	16.5	32248	22	ABA20412	Human nervous syst
C 39	196.4	16.5	32248	22	AAK37122	Human musculoskele
C 40	196.4	16.5	32248	22	AAK26795	Human genomic DNA
C 41	196.4	16.5	34658	22	AAK69489	Human immune/haema
C 42	196.2	16.5	1376	21	AAK99845	Human secreted pro
C 43	196.2	16.5	2233	22	AAK77256	Human immune/haema
C 44	196	16.5	54548	21	AAK45596	DNA sequence of th
C 45	195.8	16.5	16183	22	AAK74819	Human immune/haema

ALIGNMENTS

RESULT 1
ID AAF31109 standard: cDNA; 18596 BP.
AC AAF31109;
XX AAF31109;
DT 27-APR-2001 (first entry)
DE Thymidylate synthase coding sequence.
KW Analyte-binding enzyme; analyte analysis; ss.
OS Homo sapiens.
PN WO200102600-A2.
XX WO200102600-A2.
PD 11-JAN-2001.
XX 11-JAN-2001.
PF 30-JUN-2000; 2000WO-US18057.
PR 06-JUL-1999; 99US-0347878.
PR 06-DEC-1999; 99US-0457205.
XX (GREAT) GEN ATOMICS.
PA Thymidylate synthase
PI Human thymidylate
PI Human DNA sequence
XX Human musculoskele
DR Human immune/haema
XX Human reproductive
PT DNA encoding novel
PT Human immune/haema
PT Human immune/haema

Assaying method, useful for prognosis and diagnosis of disease,
comprises contacting sample with a mutant analyte-binding enzyme and
detecting binding -

PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225757.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226581.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
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PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
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PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
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PR 14-SEP-2000; 2000US-0233063.
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PR 21-SEP-2000; 2000US-0234223.
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PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.

PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
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PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-483426/52.

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -

PS Disclosure; SEQ ID NO 28083; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

PR	29-SEP-2000;	2000US-0236368.
PR	29-SEP-2000;	2000US-0236369.
PR	29-SEP-2000;	2000US-0236370.
PR	02-OCT-2000;	2000US-0236802.
PR	02-OCT-2000;	2000US-0237037.
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PR	17-NOV-2000;	2000US-0249211.
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PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250161.
PR	05-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.

XX	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT	useful for preventing, diagnosing and/or treating cancers and
PT	metastasis -
PT	
XX	Dislosure; SEQ ID NO 21686; 3071pp + Sequence Listing; English.
XX	
PS	
XX	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC	amino acid sequences given in AM821170 to AM91921. (I) have cytostatic
CC	activity, and can be used in gene therapy and vaccine production. (I)
CC	proteins and polynucleotides may be used in the prevention, diagnosis and
CC	treatment of diseases associated with inappropriate (I) expression. For
CC	example, they may be used to treat disorders associated with decreased
CC	expression by rectifying mutations or deletions in a patient's genome
CC	that affect the activity of (I) by expressing inactive proteins or to
CC	supplement the patients own production of (I). Additionally, (I)
CC	polynucleotides may be used to produce the secreted (I), by inserting
CC	the nucleic acids into a host cell and culturing the cell to express the
CC	protein. (I) proteins and polynucleotides may be used to prevent,
CC	diagnose and treat immune/hematopoietic-related diseases, especially
CC	cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC	to AAK87894 represent human immune/hematopoietic antigen genomic
CC	sequences from the present invention. AAK54942 to AAK54950 and AM821169
CC	represent sequences used in the exemplification of the present invention.
XX	
XX	Sequence 37449 BP; 11842 A; 7890 C; 7531 G; 10186 T; 0 other

Query Match	17.2%;	Score 204.2;	DB 22;	Length 37449;
Best Local Similarity	74.9%;	Pred. No. 1.2e-26;		
Matches 317; Conservative	0;	Mismatches 80;	Indels 26;	Gaps 4;

Qy	1	gatcgcccaactgacctcagctgggtgagagcgagaactctggtccaataaaaaaa	60
Db	23313	gATCGGCCCACTGCATCCAGCCTGGCGCAGACGCGAGACTGTCTCAAAAAA	23254
Qy	61	aaa --- aaagccgcgaaggctcaacaaaaaacctcgaaaagccctggcggtctttt	116
Db	23253	RAAAAAGAAGTGTAATAAAGCTTCATAGATTATCATCCAGACAATAATTATCAGTATTT	23194
Qy	117	tt	176
Db	23193	ACCATGTGTTCTTTTTTTTTTTTWTGAGAGAGTCTCGTCTGTGCGCCAGGCTGAGTGCAG	23134
Qy	177	tggtcgatcttgctcactgaaacctctgctcccaggttcaaagcaattctcttgctc	236
Db	23133	TGGCATGATCTCGGCTCACTGAAGCTCCACCTCCAGGTCACAGGATTCTCCTGCC TC	23074
Qy	237	agcctcccaagta-----gccaccgcgccaagctaatttttgtant	277
Db	23073	AGCCTCCAGGTGACTGGAAC TACAGGCACCCGCCACCATGCTGGCTAAATTTTGTATT	23014
Qy	278	tttaetgacaaggggtttcaaatgtcttcagactggtctingaaactcctgacctcag	337
Db	23013	TTTAGTAGAGAC--GGGGTTTACACACATTTGGTCAGTTGGTCTCAAACCTCTGACCT--T	22957
Qy	338	gtgattcacaccgcctcgcccccaaaagtactaggattacagcpgttagccacgcgtcc	397
Db	22956	G TGATACGCCCGCTCGGCTCCCAAAAGTGTGGGATTACAGGCATGAGCACCTGGCCCC	22897
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XX	
XX	
XX	
DT	06-NOV-2001 (first entry)
Y	


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Db 2189 ttgtcccgctgacctcccaagtgtggtattacaggtatgagccacatgcccggcc 2248
QY 402 cctgagcggttttaatacaagttagaaaag 430
Db 2249 aagtatccttttaataacttggataaag 2277

RESULT 13
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ID AAK79760 standard; DNA; 20601 BP.
XX
AC AAK79760;
XX
DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34572.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytotstatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WC200157182-R2.
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PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 22-AUG-2000; 2000US-0226681.
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PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0232080.
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PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2002, 16:37:26 ; Search time 5000.16 Seconds
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Title: US-09-963-333-7
Perfect score: 1187
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No. Score Match Length DB ID Description

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DEFINITION							1186 bp DNA linear PRI 06-NOV-2001
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
MEDLINE							
COMMENT							

ALIGNMENTS

HUMTS	HUMTS	1186 bp	DNA	linear	PRI 06-NOV-2001
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
MEDLINE					
COMMENT					

[illegible]


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; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-669A-17

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	Query Match	25.2%;	Score 387.4;	DB 4;	Length 35100;
	Best Local Similarity	63.5%;	Pred. No. 1.1e-92;		
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QY	175	cgcgctccgcgcgcaggagctgcagtacctggggcagatccaacatactccctgcctc	234		
Db	20963	GCTGAGACGCCCCACGAGGAACCTCAGTATCTCAGGCAGTTGAGGGAAATTTGTGCGGT	20904		
QY	235	ggcgtcagaagaagcagccgcgcggcacccgcacccttcgstattcgcgatcagcgcg	294		
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QY	295	cgcctacagcctgagagatgaattccctctgctgcacaaccaaaocgtgttcttgaaaaggt	354		
Db	20843	AGGTATAGTCTCGCGGACCACTTCCCTTACTAACCAAGAAGCGGTGTATTGGCAGGC	20784		
QY	355	gttttgaggagtgctgctgtgtttatcaagggtatccaaactgctaagaagcgtctctcc	414		
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QY	415	aaggagtgaaaaactcgtggatgcacaatgatcccgagacttttgtgacagcctggattc	474		
Db	20723	ACAGNGTTCAGATATGGGACAAAATGCTCCAGGAGTTCCTGGCGGGCGGGCGCTG	20664		
QY	475	tccaccagaagaaggggacttgggccagtttatggcttccagttggaggcattttggg	534		
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QY	535	gcagaatacagagatatggaatcagattattcaggaacagggagttgaccaactgcacaaga	594		
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Db	20543	ATTGTGGATTATAAATAAATAATCCGCACGATAGAGATCAATATGTCGCGTGGAC	20484		
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Db	20303	AGACCGGGGATTTATTCACGTTGGGAGTAGCCCACATCFACAAAAACGCTATAGAG	20244		
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RESULT 6
US-09-230-371A-17/c
; Sequence 17, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; TITLE OF INVENTION: US$ THEREOF
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 35100
; TYPE: DNA
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-17

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[illegible]

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3479 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-7

Query Match 7.98; Score 121.2; DB 4; Length 3479;

Best Local Similarity 56.88; Pred. No. 1.7e-22;
Matches 268; Conservative 6; Mismatches 194; Indels 4; Gaps 3;

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QY 638 tcattgctgctgggaatccaagagattctctctgctgctgctgctccatgcacatgcc 697
DB 1848 TCGTATCTGCATGGAATCCACAGAAATTTGATACAAATGCGACTTCGCGCTTGTACATCCA 1789
QY 698 tctgcagattctatgttgaaactgagctgctgcagctgacagagatcgaggag 757
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QY 996 gattgaaggggtacaaatccgaaatcccaactatttaaaatggaaatggctgttag 1047
DB 1490 AATTGTTGACTATGATACATCCAGCMATAAAGCTCCMATAGCAKGTGAG 1439

RESULT 9

US-09-265-315-7/c
; Sequence 7, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:

APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3479 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-265-315-7

Query Match 7.98; Score 121.2; DB 4; Length 3479;

Best Local Similarity 56.88; Pred. No. 1.7e-22;
Matches 268; Conservative 6; Mismatches 194; Indels 4; Gaps 3;

QY 578 ttacccaactcgaagagtgattgacaccatcaaaacccctgagcagagagaatca 637
DB 1908 TTGATCACTTAAACAGTATTGACAAATTAAGCAATTAATCCAGATTCAGGCGACACA 1849
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RESULT 13
US-08-483-533-37
Sequence 37, Application US/08483533
Patent No. 6172047
GENERAL INFORMATION:
APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method for Treating Tumorigenic
TITLE OF INVENTION: Diseases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483.533
FILING DATE: 07-MAR-95
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/861,233
FILING DATE: 31-MAR-92
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 28097/32742
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300

[illegible]

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 QY 553 gaatcagattattcaggacagggaggtgacaaactgcaaaagagtgattgacacccatcaaa 612
 Db 466 gacgagactacagcggcgaaggatcgacacagctgcgcccagtgatcgacacccatcagg 525
 QY 613 acaaacctcagcagaagaatacatcattgctgttggaaatccaaagagatcttctctg 672
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 Db 586 atggccctgcccgtgcactctgtggcgagttttacgtctccgagaagcgcggtgag 645
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 Db 646 ctttgcgtccagctataccagaagaagcagacatggcctggcgctacccttcaacatc 705
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 Db 706 gctcctatgcctgtccaccacatgattgcccattgtgacgggtctgaagcggcgac 765
 QY 847 ttatacacatttggagatgacatatattacatgaatcacatcagccactgaaaatt 906
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 Db 886 atcgaggacttcgcttcgaggacttccagatagtcgactacataatccatccacaaaatc 945
 QY 1027 aaaaatggaatgctgttag 1047
 Db 946 caaatggacatggccgtgtag 966

RESULT 14
 AAA78156/c
 ID AAA78156 standard; cDNA; 346 BP.
 XX AC
 AC AAA78156;
 XX XX
 XX 14-NOV-2000 (first entry)
 XX cDNA encoding human colon tumour polypeptide, SEQ ID NO:443.
 XX Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
 KW immunotherapy; diagnosis; progression; ss.
 XX OS
 XX Homo sapiens.
 XX WO200037643-A2.
 XX 29-JUN-2000.
 XX 23-DEC-1999; 99WO-US30909.
 XX 23-DEC-1998; 98US-0221298.
 PR 02-JUL-1999; 99US-0347496.
 PR 22-SEP-1999; 99US-0401064.
 PR 19-NOV-1999; 99US-0444242.
 PR 02-DEC-1999; 99US-0454150.
 XX (CORI-) CORIXA CORP.
 XX Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk J;
 PI Wang T, Yuqiu J;
 XX WPI; 2000-442671/38.
 XX

PT New colon tumor polypeptides used to inhibit the development of cancer, especially colon cancer, and for diagnosing and monitoring the progression of the cancer -
 PT Claim 1; Page 218; 229pp; English.
 XX Sequences AAA77722-A78199 represent 478 cDNAs encoding proteins or portions of proteins which are associated with human colon tumours.
 CC The invention also specifically discloses 8 human colon tumour proteins (AAB11897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing such polypeptides may be used in vaccines that target tumour cells, especially colon tumour cells, thereby inhibiting the development of cancer. T-cells specific for the polypeptide expressed by the APC are used to remove tumour cells from biological samples, especially blood or fractions thereof. The sample or the isolated T-cells specific for the polypeptide can then be used to inhibit cancer development. CD4+ and/or CD8+ T-cells from a patient may be incubated with a polypeptide or nucleic acid of the invention, or an APC expressing such a polypeptide, to cause the proliferation of specific T-cells. The T-cells can be cloned and then administered back to the patient to inhibit cancer development. Nucleic acids encoding the polypeptides and antibodies against the polypeptides may be used to determine the expression level of a tumour protein of the invention, and therefore to determine whether cancer cells are present. Such diagnostic methods may also be used to monitor the progression of a cancer by repeating the processes at time intervals, and comparing the current result to previous results. The present sequence represents a cDNA encoding a human colon tumour polypeptide.
 XX Sequence 346 BP; 104 A; 79 C; 56 G; 107 T; 0 other;
 SQ

Query Match 22.1%; Score 339.6; DB 21; Length 346;
 Best Local Similarity 98.8%; Pred. No. 8.8e-79;
 Matches 342; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1007 acaatccgcatcccaactattaaatggaaatggctgttaggtgtcttcaaaagagctc 1066
 Db 346 ACAATCCGCACTCAACTATTAAATGGAAATGGCTGTAGGTGCTTCAAAAGAGCTT 287
 QY 1067 gaagatatgtctagctcttaggggttggtggtgagatccgaggtataaagtcttttgt 1126
 Db 286 GAAGGATATGTCATCTTTAGGGGTGGGCTGGATGCCGAGGTAAAGTCTTTTGTCT 227
 QY 1127 ctaaaagaagaagaactagctcaaaatctgcgtgacctatcagttattatttta 1186
 Db 226 CTAAAGAAAGAAAGGAACACTAGTCAAAAATCTGCGTGACCCATCAGTTATTATTTTA 167
 QY 1187 aggatgttgccactggcaaatgttaactgtgccagttcttccataataaaagctttgag 1246
 Db 166 AGGATGTGGCACTGGCAAAATGTAAGTGGCCAGTTCTTCCATAATAAAGGCTTTGAG 107
 QY 1247 ttaactcactgaggggtatctgacaatgtgaggttatgaacaagtgagagaatgaat 1306
 Db 106 TTAAGTCACTGAGGTTATCTGACAATGCTGAGGTTATGAAACAAGTGAGGAGTAAT 47
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 Db 46 GTATGTCTCTTAGCAAAAACATGTATGTGCAATTCATATCCACGT 1

RESULT 15
 AAI28894/c
 ID AAI28894 standard; cDNA; 346 BP.
 XX AC
 AC AAI28894;
 XX XX
 XX 12-OCT-2001 (first entry)
 XX Colon tumour related determined cDNA sequence for clone 31975.
 DE Human; immunotherapy; diagnosis; colon cancer; colon tumour;
 KW

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

REMARK NIH-MGC Project URL: <http://mqc.nci.nih.gov>
USA

COMMENT:

Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
nisc.mgc@nih.gov

Stevechenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, S., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurgueon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAL plate: 4 Row: h Column: 10

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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 298 a 253 c 217 g 318 t 3 others
ORIGIN

Query Match 58.2%; Score 1048; DB 9; Length 1089;
Best Local Similarity 99.0%; Pred. No. 2.le-225;
Matches 1073; Conservative 2; Mismatches 7; Indels 2; Gaps 2;

QY 432 ggaatgcaatggatcccgagactttttgacagcctgggattctccaccagagaagaagg 491
Db 1083 GGATGCCAATGGAYCCCGAGAC-TTTTGGACAGCCT-GGATTTCTCCACGACAGAGAAGA 1026

QY 492 ggacttggggccagctttatggcttccagtgaggagcattttggggcagaatacacagatat 551
Db 1025 GGACTTGGCCCCAGTTTATGGCTTCCAGTGAGGAGCATTTTGGGGCAGAAATACAGAGATAT 966

QY 552 ggaatcagattattcagggacagggaggttgaccactcgaagagtgattgacacacataca 611
Db 965 GGAATCAGATTANTCAGGACAGGGAGTTGACCAACTGCAAGAGAGTGATTGACACCATCAA 906

QY 612 aaccaaccctgcacagagaagaataatcatgtgcgcttggaatcccaagagattctcct 671
Db 905 AACCAACCCCTGACACAGAGAATAATCATATGCGCTTGGAAATCCAGAGATCTTCCCTCT 846

QY 672 gatgagctgtcctcagtcgcatgcccctgtccagttctatgtgtgaacagtgagctgtc 731
Db 845 GATGGCGTGCCTCCATGCCATGCCCTCTGCCAGTTCTATGTGTGGTGAACAGTGAGCTGTC 786

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Db 785 CTGCCAGCTGTACCAGAGATCGGGAGACATGGGCTCGGTGCTGCTTTCAACATCGCACA 726

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Db 725 STACGCCCTGCTCACGTACATGATGCGACATCAACGCGGCTGAAAGCCAGGTGACTTTAT 666

QY 852 acacacttgggagatgcacataattacttaactgaatcacatcgagccactgaaatcacgct 911
Db 665 ACACACTTTGGAGATGCACATATTTACCTGAATCACATCGAGCCACTGAAATTCAGCT 606

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Db 605 TCAGCGAGAACCCAGACTTTTCCAAAGCTCAGGATTTCTCGAAAAAGTTGAGAAAATTTGA 546

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QY 1152 aaatctgtccgtgacctatcagttatttaatttttaaggatgtttgcacatggcaaatgtaa 1211
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QY 1212 ctgtgccagttctttccataataaaaggcttttgagtttaactcactgaggggtatctcgaca 1271

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QY 1332 atgtgcatttcaatcccaogtacttataaaagaagtttgggtgaatttcaacaagctatttt 1391
Db 185 ATGTGCAATTCATCCACGCTACTTATAAAGAGGTTGGTGAATTTTCACAAGCTATTTT 126
QY 1392 ggaatattttagaataattttaagaatttcaacagctattccctcaaatctgagggagct 1451
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QY 1452 ggaataaccatcatcatgtagtgagtggtttagaacttttaagttgttttttatgt 1511
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QY 1512 ttgc 1515
Db 5 TTGC 2

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DEFINITION Prime, mRNA sequence.
ACCESSION AL572496
VERSION AL572496.1 GI:12930822
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 294 a 251 c 214 g 309 t 9 others
ORIGIN

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Query Match 67.9%; Score 1043.6; DB 9; Length 1077;
Best Local Similarity 97.9%; Pred. No. 2e-224;
Matches 1049; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 438 caatggatcccgagactttttgacagcctgggattctccaccagagaagaaggagactt 497
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QY 515 tccatgaggagcatttggggcagatacagagatatggaatcagattattcagacagg 574
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 QY 575 gaggtagcaactgcaagagtgattgacacccatcaaaacccacccctgacagacagaagaa 634
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 QY 635 tcatcatggtggtggaatccaagagattctcctctgatgagcgtcctccatgcagtg 694
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 QY 695 cccctgtccagttctatgtgtggaacagtgagctgtcctgcagctgacacagagatcgg 754
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 VERSION AL562750.1 GI:12911478
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1021)
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 Bp 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact : Feng liang life
 Technologies, a division of Invitrogen 9800 Medical Center

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com*
 BASE COUNT 276 a 230 c 203 g 307 t 5 others
 ORIGIN

Query Match 61.5%; Score 945.2; DB 9; Length 1021;

Best Local Similarity 98.0%; Pred. No. 2.9e-202;
Matches 964; Conservative 3; Mismatches 16; Indels 1; Gaps 1;

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 QY 589 caaagagtgattgacacatcaaaacccctgcacgacagaagaatcatcatgtcgct 648
 Db 924 CAAAGAGTGATTMACACCATCAAAACCAACCCCTRACACAGAGAATCATGTGCGCT 865
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 QY 828 gggcctgaagccagtgactttatacacactttgggagatgcacatatattacotgaatca 887
 Db 684 GGGCTGAAGCCAGGTGACTTTATACACACTTTGGGAGATGCACATATTTACCTAAATCA 625
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 QY 1008 caatccgcacccaactattaaaatggaaatggcgttttaggtgctttcaaaaggagctg 1067
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RESULT 15
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VERSION AL578646.1 GI:12942922
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 906)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 131 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 256 a 200 c 183 g 264 t 3 others
ORIGIN
Query Match 57.8%; Score 887.4; DB 9; Length 906;
Best Local Similarity 99.1%; Pred. No. 2.8e-189;
Matches 899; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
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DB 7 TTATAWG 1

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Search completed: July 26, 2002, 15:13:16
Job time: 26880 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2002, 09:55:26 ; Search time 5000.15 Seconds
(without alignments)
6428.426 Million cell updates/sec

Title: US-09-963-333-6
Perfect score: 1536
Sequence: 1 ggggggggggggaccacttg.....ataataaagaagtgtctgc 1536

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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- 2: gb_htg.*
- 3: gb_in.*
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- 7: gb_ph.*
- 8: gb_pl.*
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- 27: em_sts.*
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- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

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4	1494.8	97.3	3298	6	AX281791	X02308 Human mRNA
5	1484.6	96.7	1569	9	BC013919	BC002567 Homo sapi
6	942	61.3	942	6	AX069365	AX281791 Sequence
7	728	47.4	840	6	AB077208	BC013919 Homo sapi
8	711.4	46.3	986	10	BC020139	AX069365 Sequence
9	697.6	46.0	961	10	MUTHSM	AB077208 Homo sapi
10	697.8	45.4	1598	10	RATHYSYN	BC020139 Mus muscu
11	634.2	41.3	1349	10	MUSPSTSA	M13019 Mouse thymi
12	613.2	39.9	18596	6	AR144965	L12138 Rattus norv
13	613.2	39.9	18596	6	AX050451	M30774 Mouse thymi
14	613.2	39.9	18596	6	AX330682	AR144965 Sequence
15	613.2	39.9	18596	6	AX330906	AX050451 Sequence
16	613.2	39.9	18596	6	AX335755	AX330682 Sequence
17	613.2	39.9	18596	9	HUMTS1	AX335755 Sequence
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35	391.8	25.5	43658	14	HSV3PRGEN	M13190 Herpesvirus
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37	390.2	25.4	3336	14	HSVT	M64346 Herpesvirus
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ALIGNMENTS

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LOCUS	Sequence 1 from patent US 6087489.					
DEFINITION	Sequence 1 from patent US 6087489.					
ACCESSION	AR103889					
VERSION	AR103889.1	GI:12815477				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1536)					
AUTHORS	Dean, N.M.					
TITLE	Antisense oligonucleotide modulation of human thymidylate synthase expression					
JOURNAL	Patent: US 6087489-A 1 11-JUL-2000;					
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Qy 121 tcgagctccgcgcgcgccttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
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BC002567
LOCUS
DEFINITION Homo sapiens, thymidylate synthetase, clone MGC:1590 IMAGE:3138877,
mRNA, complete cds.
ACCESSION BC002567
VERSION BC002567.1 GI:12803482
KEYWORDS MGC.

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ACCESSION M13019.1 GI:202029
VERSION thymidylate synthetase.
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ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 961)
AUTHORS Petryman, S.M., Rossana, C., Deng, T., Vanin, E.F. and Johnson, L.F.
TITLE Sequence of a cDNA for mouse thymidylate synthase reveals striking
similarity with the prokaryotic enzyme
JOURNAL Mol. Biol. Evol. 5, 313-321 (1988)
MEDLINE 88174353
COMMENT Draft entry and printed copy of the sequence [1] kindly provided by
L.F. Johnson, 29-AUG-1986.
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VERSION	AR144965.1	GI:15106832	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 18596)		
AUTHORS	Johnson,W.G. and Stenroos,E.Scott.		
TITLE	Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factors		
JOURNAL	Patent: US 6210950-A 11 03-APR-2001;		
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		Indels 6;	Gaps 1;
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Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 4521 a 3991 c 4479 g 5605 t
ORIGIN

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Best Local Similarity 90.6%; Pred. No. 9.8e-117;
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DB 15690 AGACTTTTCAGATTTGAGGGTACAAATCCGCATCCCACTATTAATAATGGAATGGCTGTGTTA 15749

QY 1047 ggggtcttccaaagctcgaaggtatgtcagcttttaggggttggctggatgcg 1106
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DB 16110 TATTTTAAGAATTTCAAGCTATTCCTCAAACTGAGGAGCTGAGTAACACCATCGA 16169

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QY 1521 taaagaagttctgc 1536
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LOCUS
DEFINITION Sequence 1415 from Patent WO0194629.
ACCESSION AX330906

AX330906.1 GI:18103885
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrihan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 1415 13-DEC-2001;
FEATURES Avalon Pharmaceuticals (US)
Location/Qualifiers
source 1..18596
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 4521 a 3991 c 4479 g 5605 t
ORIGIN

Query Match 39.9%; Score 613.2; DB 6; Length 18596;
Best Local Similarity 90.6%; Pred. No. 9.8e-117;
Matches 667; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

QY 807 gtacatgatgcgcacatcacgagcctgaagccaggtgactttatcacacactttgggaga 866
DB 15510 GAACCTTTGTTGATCACAATCTGTTGTTTTCACGGACATGAGGACAAATTACAACAG 15569

QY 867 tgcacattatcacctgaatcacatcacgagcctgaagccaggtgactttatcacacactttgggaga 926
DB 15570 GTCGTACAAATATGCGCAAAATATGCGCTTATTTGTTTTCACGGACATGAGGACAAATTACAACAG 15629

QY 927 acccttccaaagctcaggaattcttgcgaaggttgagaaattgagcttcaaaagtga 986
DB 15630 ACCCTTCCAAAGCTCAGGATCTTCGAAAAGTTGAGAAAATTTGATGACTTCAAAAGCTGA 15689

QY 987 agactttcagatgaaggtacaatccgcacatccacactattaaaatggaaatggctgttta 1046
DB 15690 AGACTTTTCAGATTTGAGGGTACAAATCCGCATCCCACTATTAATAATGGAATGGCTGTGTTA 15749

QY 1047 ggggtcttccaaagctcgaaggtatgtcagcttttaggggttggctggatgcg 1106
DB 15750 GGGTCTTTTCAAGAGCTCGAAGGATTTGTCAGTCTTTAGGGGTGGCTGGATGCCG 15809

QY 1107 aggttaaaagttcttttgcctaaagaaaggaactaggtcaaaaactctccgtgac 1166
DB 15810 AGGTAAAGTTCTTTTGGCTTAAAGAAAGAAAGGAACTAGGTCAAAATCTGTCGTGAC 15869

QY 1167 ctatcagttattatatttgaaggtgtgccaactggcaaatgtaactgtgcagttcttt 1226
DB 15870 CTATCAGTTATTATTTTAAAGGATTTGCCACTGGCAAAATGTAACTGTGCCAGTTCITT 15929

QY 1227 ccataataaaggcttgagttgaactgaaggtatctgacaactgtcgaaggttatgaa 1286
DB 15930 CCATAATAAAGGCTTGAAGTTAACTGAAGGATTTGCGACTGGCAAAATGTAACTGTGCCAGTTCITT 15989

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2002, 17:46:36 ; Search time 77.68 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	297.8	25.1	1536	3	US-09-089-195-1
3	191.8	16.2	14747	4	US-09-608-285A-42
4	191.8	16.2	15977	4	US-09-608-285A-59
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8	189	15.9	35060	3	US-08-814-095-7
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c 11	188.8	15.9	87350	3	US-08-781-891-79
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13	187.2	15.8	72604	4	US-09-268-992-7
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24	183.6	15.5	619	4	US-09-385-982-358
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c 30	181.6	15.3	87350	3	US-08-781-891-79	Sequence 79, Appli
c 31	181.4	15.3	4038	3	US-08-969-125-8	Sequence 8, Appli
c 32	180.8	15.2	1811	1	US-08-848-252-1	Sequence 1, Appli
c 33	179.4	15.1	841	5	PCT-US93-06251-80	Sequence 80, Appli
c 34	179.4	15.1	841	5	PCT-US93-06251-81	Sequence 81, Appli
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c 44	178.6	15.0	2562	2	US-08-436-771-8	Sequence 8, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 11, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18596
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-11

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; Sequence 59, Application US/09608285A
; Patent No. 6335013

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Best Local Similarity	77.1%;	Pred. No. 1.8e-25;		

[illegible]

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US-08-814-095-7
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.000666
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including ACHE
; DESCRIPTION: promotor, ACHE gene and ARS gene"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7q22
; FEATURE:
; NAME/KEY: promotor
; LOCATION: 4089..22464
; OTHER INFORMATION: /function= "ACHE Promotor"
; OTHER INFORMATION: /standard_name= "ACHE Promotor"
; FEATURE:
; NAME/KEY: exon
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; NAME/KEY: exon

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OY	178	ggtcgagattctggctcacctgaaacctctgtcccccaggttcacaagcaaatcttctgctcca	237		
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1 RESULT 10
2 US-09-154-602-6/c
3 ; Sequence 6, Application US/09154602
4 ; Patent No. 6300472
5 ;
6 GENERAL INFORMATION:
7 ;
8 ; APPLICANT: Hillman, Jennifer L.
9 ; APPLICANT: Lal, Preeti
10 ; APPLICANT: Corley, Neil C.
11 ; APPLICANT: Shah, Purvi
12 ; TITLE OF INVENTION: RAB PROTEINS
13 ; NUMBER OF SEQUENCES: 9
14 ; CORRESPONDENCE ADDRESS:
15 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
16 ; STREET: 3174 Porter Dr.
17 ; CITY: Palo Alto
18 ; STATE: CA
19 ; COUNTRY: USA
20 ; ZIP: 94304
21 ;
22 COMPUTER READABLE FORM:
23 ; MEDIUM TYPE: Diskette
24 ; COMPUTER: IBM Compatible
25 ; OPERATING SYSTEM: DOS
26 ; SOFTWARE: FastSeq for Windows Version 2.0
27 ; CURRENT APPLICATION DATA:
28 ; APPLICATION NUMBER: US/09/154,602
29 ; FILING DATE:
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER: 08/916,901
32 ; FILING DATE:
33 ; ATTORNEY/AGENT INFORMATION:
34 ; NAME: Billings, Lucy J.
35 ; REGISTRATION NUMBER: 36,749
36 ; REFERENCE/DOCKET NUMBER: PF-0367 US
37 ; TELECOMMUNICATION INFORMATION:
38 ; TELEPHONE: 415-855-0555
39 ; TELEFAX: 415-845-4166
40 ; INFORMATION FOR SEQ ID NO: 6:
41 ; SEQUENCE CHARACTERISTICS:
42 ; LENGTH: 2713 base pairs
43 ; TYPE: nucleic acid
44 ; STRANDEDNESS: single
45 ; TOPOLOGY: linear
46 ;
47 US-09-154-602-6

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Query Match	15.9%;	Score 188.8;	DB 4;	Length 2713;
Best Local Similarity	81.9%;	Pred. No. 5.4e-25;		
Matches 249; Conservative	0;	Mismatches 34;	Indels 21;	Gaps 2;
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Db 1238 TTTTAGTAGACAGAGGGTTTCAACATGTTGGCCAGGCTGGTCTGGAACCTCTGACCTCA 1179
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RESULT 11

US-08-781-891-79
; Sequence 79, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620-tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-781-891-79

Query Match 15.9%; Score 188.8; DB 3; Length 87350;
Best Local Similarity 69.9%; Pred. No. 6.6e-25;
Matches 320; Conservative 0; Mismatches 108; Indels 30; Gaps 4;

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QY 332 cctcaggtgatccacccgctcgcccccacaaagtaactagattacaggtgagccacc 391
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Db 30109 GCTCAGGCAATCCACCCCGCGCTCCCAAAATTTGTGGATTACAGGCTGAGCCACCA 30168
QY 392 gctccagcgcctcgcggtttttaatacaagtagaanaa 429
Db 30169 GTGCTGCCAGAGAGAGATATTTAATGAAAAATAATA 30206

RESULT 12

US-07-906-871-15/c
; Sequence 15, Application US/07906871
; Patent No. 5340739
; GENERAL INFORMATION:
; APPLICANT: Stevens, Richard L.
; APPLICANT: Avraham, Shalom
; TITLE OF INVENTION: HEMATOPOIETIC CELL SPECIFIC
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY ELEMENTS OF SERGLYCIN AND
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue, N.W., Suite 300
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,871
; FILING DATE: 19920103
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/816,289
; FILING DATE: 03 JAN 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/635,544
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: PCT/US89/03051
; FILING DATE: 13-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/224,035
; FILING DATE: 13-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0627,2830004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)833-7533

OY 1521 taagaagtgtctgc 1536
|||||
Db 16230 TAAAGAAGTGTCTGC 16245

Search completed: July 26, 2002, 15:37:26
Job time: 24120 sec

QY 867 tgacacattattacacgaatcagcagccactgaaattcagcttcagcagcagccag 926
 Db 15570 GTCGTACAAATATGCGAATAATGCGCTTATTTTGTGTTTACCTCAGCAGACCCAG 15629
 QY 927 accttcccaagctcagcagcttcgaaagttagaataattgatcactcgaagtga 986
 Db 15630 ACCCTTCCCAAGCTCAGGATCTTCGAAAAGTTGAGAAAATTTGATGACTTCAAAGCTGA 15689
 QY 987 agacttcagattgaagggtacacatccgacacacactattataaaggaaatgctgttta 1046
 Db 15690 AGACTTCAGATTATGCGAATAATGCGCTTATTTTGTGTTTACCTCAGCAGACCCAG 15629
 QY 1047 ggggtcttcaaggagctcgaagatattgtcagctcttaggggttgagctgcgcg 1106
 Db 15750 GGGTCTTCAAGGAGCTCGAAGATATTGTCAGTCTTTAGGGGTGGGCTGGATGCG 15809
 QY 1107 aggttaaaagtcttttgccttaaaagaagaagacactaggttcaaaatctgtccgtgac 1166
 Db 15810 AGGTAAAGTCTTTTGTCTTAAAGAAAAGAACTAGGTCAAAAATCTGCTCGTGAC 15869
 QY 1167 ctatcagttattattttaaagattgttgcactgaggttatctgacaatgtgaggttatgaa 1226
 Db 15870 CTATCAGTTATTATTTTAAAGATGTTGCCACTGGCAATGTAATGTAATGTAATGTT 15929
 QY 1227 ccataataaaagcttttgagtttaactcactgaggttatctgacaatgtgaggttatgaa 1286
 Db 15930 CCATAATAAAAGGCTTTGAGTTAACTCACTGAGGATATCTGACATGCTGAGGTATGAA 15989
 QY 1287 caaagttagagagaatgaaatgtatgtctcttagcaaaacacatgtatgtcattcaatc 1346
 Db 15990 CAAAGTGAGGAGAATGAAATGTATGTCTCTTAGCAAAACATGTATGTCAATTCATC 16049
 QY 1347 ccagctactataaagaaggttggtgaatttcaaacactatttttggaaatttttsgaa 1406
 Db 16050 CCAGCTACTTATAAAGAGGTTGGTGAATTTTCAACAGCTATTTTGGAAATTTTGTAGAA 16109
 QY 1407 tatittagaatttcaagctattccctcaaatctgagggagctgagtaacacacatcga 1466
 Db 16110 TATTTTAAAGATTTCAAGCTATTCCCTCAATCTGAGGGAGCTGAGTACACATCGA 16169
 QY 1467 tcatgtatgagtggtgttatgaaactttaA-----agttgttttatgttctataa 1520
 Db 16170 TCATGATGATGAGTGTGTTATGAACCTTAAAGTTATAGTTGTTTATATGTTCTATAA 16229
 QY 1521 taaagaagtgtctgc 1536
 Db 16230 TAAAGAAGTGTCTGC 16245

RESULT 13
 LOCUS AX050451 18596 bp DNA linear PAT 12-JAN-2001
 DEFINITION Sequence 11 from Patent WO0071754.
 ACCESSION AX050451
 VERSION AX050451.1 GI:12226657
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 18596)
 Johnson, W.G. and Stearns, E.S.
 Methods for diagnosing, preventing, and treating developmental
 disorders due to a combination of genetic and environmental factors
 Patent: WO 0071754-A 11 30-NOV-2000;
 University of Medicine and Dentistry of New Jersey (US)
 FEATURES
 Location/Qualifiers
 source 1..18596
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 4521 a 3991 c 4479 g 5605 t
 ORIGIN

Query Match 39.9%; Score 613.2; DB 6; Length 18596;
 Best Local Similarity 90.6%; Pred. No. 9.8e-117;
 Matches 667; Conservative 0; Mismatches 63; Indels 6; Gaps
 QY 807 gtacatgatgcgcacatcacccggcctgaagccaggtgactttatcacacattgggaga 866
 Db 15510 GAACCTTTTGATCAGATCTGTGACTTGTTCACGGACATGAGGAGCAATACACAG 15569
 QY 867 tgcacatatatttaoctgaatcactgagccactgaaattcagcttcagcagcagccag 926
 Db 15570 GTCGTACAAATATGCGAATAATGCGCTTATTTTGTGTTTACCTCAGCAGACCCAG 15629
 QY 927 accttcccaagctcagcagcttcgaaagttagaataattgatcactcgaagtga 986
 Db 15630 ACCCTTCCCAAGCTCAGGATCTTCGAAAAGTTGAGAAAATTTGATGACTTCAAAGCTGA 15689
 QY 987 agacttcagattgaagggtacacatccgacacacactattataaaggaaatgctgttta 1046
 Db 15690 AGACTTCAGATTATGCGAATAATGCGCTTATTTTGTGTTTACCTCAGCAGACCCAG 15629
 QY 1047 ggggtcttcaaggagctcgaagatattgtcagctcttaggggttgagctgcgcg 1106
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 Db 15810 AGGTAAAGTCTTTTGTCTTAAAGAAAAGAACTAGGTCAAAAATCTGCTCGTGAC 15869
 QY 1167 ctatcagttattattttaaagattgttgcactgaggttatctgacaatgtgaggttttt 1226
 Db 15870 CTATCAGTTATTATTTTAAAGATGTTGCCACTGGCAATGTAATGTAATGTAATGTT 15929
 QY 1227 ccataataaaagcttttgagtttaactcactgaggttatctgacaatgtgaggttatgaa 1286
 Db 15930 CCATAATAAAAGGCTTTGAGTTAACTCACTGAGGATATCTGACATGCTGAGGTATGAA 15989
 QY 1287 caaagttagagagaatgaaatgtatgtctcttagcaaaacacatgtatgtcattcaatc 1346
 Db 15990 CAAAGTGAGGAGAATGAAATGTATGTCTCTTAGCAAAACATGTATGTCAATTCATC 16049
 QY 1347 ccagctactataaagaaggttggtgaatttcaaacactatttttggaaatttttsgaa 1406
 Db 16050 CCAGCTACTTATAAAGAGGTTGGTGAATTTTCAACAGCTATTTTGGAAATTTTGTAGAA 16109
 QY 1407 tatittagaatttcaagctattccctcaaatctgagggagctgagtaacacacatcga 1466
 Db 16110 TATTTTAAAGATTTCAAGCTATTCCCTCAATCTGAGGGAGCTGAGTACACATCGA 16169
 QY 1467 tcatgtatgagtggtgttatgaaactttaA-----agttgttttatgttctataa 1520
 Db 16170 TCATGATGATGAGTGTGTTATGAACCTTAAAGTTATAGTTGTTTATATGTTCTATAA 16229
 QY 1521 taaagaagtgtctgc 1536
 Db 16230 TAAAGAAGTGTCTGC 16245

RESULT 14
 LOCUS AX330682 18596 bp DNA linear PAT 09-JAN-2
 DEFINITION Sequence 1191 from Patent WO0194629.
 ACCESSION AX330682
 VERSION AX330682.1 GI:18103660
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (sites)
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horrigan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signal

160	GGAGGACCGCAGGGGCACTGGGCACCCCTGTGCGGTTCGGCGATCGAGCGACGATACAGCCT	219
306	gagagatgaattccctctctgctgacaacaaacgtgttcttgggaagggtgttttgagga	365
220	GAGAGATGAATTCCTCTCTGCTCACAAACAAACGAGTGTCTCGGAGGGGTGTTTGGAGGA	279
366	gttgctgtggtttatcaaggagatccacaatgctaaagagctgtcttccaaggagtgaa	425
280	GTTGTGTGTGTTTATCAAGGGATCCAAAATGCTAAAGATGTTCCTCAAGGGAGTGAG	339
426	aatctggagatgccaatggatccagagacttttgacacgctgggattctccacacaga	485
340	ATCTGEGATGCCAATGAGATCCGAGATTTCTTGACAGCTTGGGATTTCTGCCCCACA	399
486	agaagggaacttgggccagtttatggcttcaccatggaggcatttggggcagaatacag	545
400	GGAAGGGGACCTGGGCCAGTTTATGTGTTTCCANTGAGGCAATTTTGGAGCAGAGTACAA	459
546	agatatggaatcagattatcagacagggaggttgaccaactgcaaaagtgattgacac	605
460	AGATATGSGATTTCAGATTACTCGGACAAAGGAGTAGACAGCTGCAAAAAGTGAATGCAC	519
606	catcaaaacaaacctgacgacacaagaatcatcattgagcctggaatccaaagatct	665
520	CATCAAAACCAACCCGTATGACAGAGAATCATCATGTGTGCGCTGGAAACCCAAAGATCT	579
666	tccctgatggcgctgcctccatgcactgcctctgcagttctatgttggtaacagtga	725
580	TCCCTGATGGCACTGCCTCCTTGGCATGCCCTCTGTCACTTCATGTGGTGAATGGGA	639
726	gctgtcctgcagctgtacccagagatcgggagacatcgggctcgtgtgccttccaacat	785
640	ACTGTCTTGCCAGCTTTACAGAGGTCAGGAGATATGGCTGGCGGTGCCCTCAACAT	699
786	gcacgtcagccctgcacgtacatgattgcgacaatacagggcgtgaagccaggtga	845
700	TGCAGCTATGCTGCTGCACCTCATATGATTCACATATCACAGGCGCTGCAGCCAGGTGA	759
846	ctttatatacaacttgggagatgcacatttaccctgaatcacatcgagccactgaaat	905
760	TTTTGTCCACACTTTGGGAGATGCACATATTACCTGNATCATATAGAGCCGCGTGAANAT	819
906	taagctcagcgagaaccagaccttcccaagctcaggtattcttcgaaagtggagaa	965
820	TCAGCTACAGCGAGAACCAAGACCTTTCGCCAAAGCTCAAAATCCTTCGAAAGTTGAGAC	879
966	aattgatgacttcaagctgaagacttccagattgaagggtacaatccgcgtaccaactat	1025
880	AATCGATGATTTCAAGTTTGAAGCTTTCAGATTGAGGGGTATTAATTCACATCAACGAT	939
1026	taaaatggaatggctgttta	1046
940	TAAATGAAATGGCTGTTTA	960

RESULT 10	
RATHYSYN	
LOCUS	1598 bp mRNA linear ROD 30-MAY-2000
DEFINITION	Rattus norvegicus thymidylate synthase mRNA, complete cds.
ACCESSION	L12138
VERSION	Li2138.1 GI:207327
KEYWORDS	thymidylate synthase.
SOURCE	Norway rat.
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 1598)
AUTHORS	Ciesla,J., Weiner,K.X., Weiner,R.S., Reston,J.T., Maley,G.F. and Maley,F.
TITLE	Isolation and expression of rat thymidylate synthase cDNA:
JOURNAL	phylogenetic comparison with human and mouse thymidylate synthases Biochim. Biophys. Acta 1261 (2), 233-242 (1995)

[illegible]

[illegible]

Db 541 GGGAGTTGACAACTGCAAAAGAGTGATTGACACACATCAAAACCAACCTGACGACAGAG 600

QY 633 aatcatcatgtgccttggaatccaagaagatcttccctgtatggcgctgcctcatgcoa 692

Db 601 AATCATATGTGGCTTGAATCCAGAGATCTTCTCTGTATGGCGCTGCTCATGCCA 660

QY 693 tgcctctgcagttctatgtgtgaacagtgagctgtcctctccagctgtaccagatgc 752

Db 661 TGCCCTCTGCCAGTTCTATGTGGTGAACAGTGAGCTGTCTGCAAGCTGTACCAGATC 720

QY 753 gggagacaatgggctcgtgtgtccttcaacatgcagctcagctcgtcctcagtcacat 812

Db 721 GGGAGACATGGGCTCGGTGTCCTTCAACATCGCCAGCTACGCCCTGCTACAGTACAT 780

QY 813 gattgcgcacatcacggcgctgaagccaggtgactttatcacac--tttgggagatgca 870

Db 781 GATTGCGCACATCAGGGGCTGAAGCCAGGTGACTTTATACACACCTTTGGGAGATGCA 840

QY 871 catattacctgaatcacatgcagccactg--aaaattcagcttcagcg--agaaccaga 927

Db 841 CATATTACCTGAATCCATCGAGCCACTGGAAAATTCAGCTTCAGCGAAGAACCCAGA 900

QY 928 ccttt-cccaactcagattctt---cgaaaagttgaaaaattgatga-cttcaag 982

Db 901 CCTTCCCAAGCTCAGGATTCCTTCCAAAAGGTTGAGAAAATTGATGACCTTCCAAG 960

QY 983 ctgaagacttt--cagattgaaggtacacatccqcatcccaactattaaaatggaaatggc 1040

Db 961 CTGAAAATTTTCAGATTGAGGGACAAATCCCGCATCATCTTTTAAATGGAAATGGG 1020

QY 1041 t 1041

Db 1021 T 1021

RESULT 14

AL515910/c

LOCUS AL515910 LFI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA001YD20 3

DEFINITION AL515910 LFI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA001YD20 3

prime, mRNA sequence.

AL515910

ACCESSION AL515910.1 GI:12779403

VERSION

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .923

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0DA001YD20"

/clone_lib="LFI_NFL011_NBC1"

/sex="male"

/issue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email :

FEATURES

source

fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 249 a 206 c 188 g 269 t 11 others

ORIGIN

Query Match 57.8%; Score 888.4; DB 9; Length 923;

Best Local Similarity 97.5%; Pred. No. 1.7e-189;

Matches 900; Conservative 10; Mismatches 12; Indels 1; Gaps

QY 570 acaggagttgacccaactgaaagtgattgacacacatcaaaaccaa--ccttgacgaca 628

Db 923 ACAGGGAGTTGACCMATCTCAAGAGTGYTTCACACCATCAAAACCAACCCCTGACAACA 864

QY 629 gaagaatcatcatgtgccttgggaatccaagagatcttctctgtatggcgctgcctcat 688

Db 863 GAAGAATCWTMATGTGCGCTTGGAAATCCAGAGMTCTTCTCTGATGSGGTGCTCCAT 804

QY 689 gccatgcctctgcagcttctatgtgtgaacagtgagctgtcctgccagctgtaccaga 748

Db 803 GCCATGCCCTCTGCCAGTTCTTTGTGTGAACAGTGWGCTGTCTTCCAGCTGTACCAGA 744

QY 749 gatcggagacatgggcctcgtgtgcctttcaacatgcgcagctacgcctgtcactcgt 808

Db 743 CATCGGAGACATGGGCTCGGTGTGCTTTCAACATCGCCCACTACGCCCKGCTAACGA 684

QY 809 acatgattgcacatcacggcgctgaagccaggtgactttatatacaactttggagatg 868

Db 683 ACATGATTGGCACAATCAGCGGCTGAAGCCAGGTGACTTTTAAACACACTTTGGGAGATG 624

QY 869 cacatattacctgaatcacatgcagccactgaaatcagcttcagcgagaaacccagac 928

Db 623 CACATATTACCTGAATCACAATCGAGCCACTGAAAATTCAGCTTCAGCGAAGAACCCAGAC 564

QY 929 ctttcccaagctcagattcttcgaaaagttcagaaaattgatcactcctaaagctgaag 988

Db 563 CTTTCCCAAGCTCAGGATTTCTCGAAAAGTTGAGAAAATTTGATGACTTCAAGCTGAAG 504

QY 989 acttcagattgaagggtacacatccgcacccaactattaaaatggaatggctgttagg 1048

Db 503 ACTTTCAGATTGAGGGTACATCCGCATCCCACTATAAATGGAATGCGTGTIAGG 444

QY 1049 gtctttcaagagctCgaaggtattgtcagttcttttaggggttggcgtggatgcgcag 1108

Db 443 GTGCTTTCAAAGGAGCTCGAAGGATATTTGTCAGTCTTTTAGGGTTGGGTGATGCCGAG 384

QY 1109 gtaaaagtctttttctctataaagaagaagaaactaggtcaaaatctgtccgtgacct 1168

Db 383 GTAAAAGTTCTTTTCTCTTAAAGAAAAGAAAGAACTAGGTCAAAAATCTGTCGGTACCT 324

QY 1169 atcagttattatttttaaggatgtgcactggcaaatgtaactgtgccagttctttcc 1228

Db 323 TTCAGTTATTAATTTTAAAGATGTTGCCACTGGCAATGTAACTGTGCGCAGTTCTTCC 264

QY 1229 ataataaagcctttgagtttaactcactgaggttatctgcacatgctgaggttatgaca 1288

Db 263 ATAATAAAGGCTTTGAGTTAACTCACTCAGGGTTTCTGACAATGCTCAGGTATTGAACA 204

QY 1289 aagtggagagaatgaaatgtatgtctcttagcaaaaaacatgtatgtcattcaatccc 1348

Db 203 AAGTGGAGAGAATGAAATGATGTCTCTTTAGCAAAAACATGTTTGTGATTTCAATCCC 144

QY 1349 acgtactataaagaaggtgtgtaattcacagctatttttgaatatatttagaata 1408

Db 143 ACGTACTTATAAAGAGGTTGTGTAATTTCAAGAGCTATTTTGGNAATATTTTAGATA 84

QY 1409 tttaagaatttcacagctattcctcctcaaatctgagggagctgagtaacaccatcgcac 1468

Db 83 TTTTAAAGATTTCAACAGTATTCCTCAATCTGAGGAGGCTGAGTNACACCATCGATC 24

QY 1469 atgatgtagagtggttatgaa 1491

Db 23 ATGATGTAGAGTCTGCTTATGAA 1

KW immunogenic; gene therapy; vaccine; colonic cancer; ss.
 XX Homo sapiens.
 OS
 PN WO200149716-A2.
 XX
 PD 12-JUL-2001.
 XX
 PF 29-DEC-2000; 2000WO-US35596.
 XX
 PR 30-DEC-1999; 99US-0476296.
 PR 10-JAN-2000; 2000US-0480321.
 PR 15-FEB-2000; 2000US-0504629.
 PR 06-MAR-2000; 2000US-0519444.
 PR 19-MAY-2000; 2000US-0575251.
 PR 29-JUN-2000; 2000US-0609448.
 PR 28-AUG-2000; 2000US-0649811.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Lodes MJ, Secretist H, Benson DR, Meagher MJ, Stolk JA;
 PI King GE, Wang T, Jiang Y;
 XX
 DR WPI; 2001-441847/47.
 XX
 PT Colon tumor associated proteins and nucleic acids useful for the
 PT prevention, diagnosis and treatment of colonic cancer -
 XX
 PS Claim 2; Page 254; 472pp; English.
 XX
 CC The present invention describes colon tumour associated proteins (I) and
 CC the polynucleotides (II) that encode them. (I) have cytostatic activity.
 CC (I) and (II) can be used in gene therapy and vaccine production. (I) and
 CC (II) may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate colon tumour associated protein (TCAP)
 CC expression, such as colonic cancer. For example, (I) and (II) may be
 CC used to treat disorders associated with decreased expression by
 CC rectifying mutations or deletions in a patient's genome that affect the
 CC activity of TCAPs by expressing inactive proteins or to supplement the
 CC patients own production of them. Additionally, (II) may be used to
 CC produce the TCAP proteins, by inserting the nucleic acids into a host
 CC cell culturing the cell to express the protein. (II) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC polymerase chain reaction (PCR) and hybridisation assays to detect and
 CC quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy. (I) may
 CC also be used as antigens in the production of antibodies against TCAPs
 CC and in assays to identify modulators of TCAP expression and activity.
 CC Anti-(I) antibodies and antagonists may also be used to down regulate
 CC TCAP expression and activity. The anti-(I) antibodies may also be used
 CC as diagnostic agents for detecting the presence of TCAPs in samples
 CC (e.g. by enzyme linked immunosorbent assay (ELISA)). AAI28460 to AAI29512
 CC and AAM24494 to AAM24523 represent nucleotide and amino acid sequences
 CC given in the exemplification of the present invention.
 XX
 SQ Sequence 345 BP; 104 A; 79 C; 56 G; 107 T; 0 other;

Query Match 22.1%; Score 339.6; DB 22; Length 346;
 Best Local Similarity 98.8%; Pred. No. 8.8e-79;
 Matches 342; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1007 acatccgcacccactattaaatggaatggctgtgttaggggtgctttcaaggagctc 1066
 |||||||
 DB 346 ACAATCGCATCCAACTATTAAATGGAATGGCTGTGTAGGGTGTCTTCAAGGAGCTT 287
 |||||||
 QY 1067 gaaggatattgtcagttcttaggggttggtggtgagtcgaggtgaaagtctcttttgc 1126
 |||||||
 DB 286 GAAGGATATTGTCACTCTTTAGGGGTGGGCTGGATGCCGAGGTAAAGTCTCTTTTGT 227
 |||||||
 QY 1127 ctaaaagaaggaactagtcacaaaatctgtccgtgacccatcagttattatttta 1186
 |||||||
 DB 226 CTAAGAGAAAGGACTAGTCTCAAAATCTGTCCGTGACCCATCAGTTATTAAATTTTA 167

QY 1187 aggatgttgcactggcgaatgtaactgtgccaagtctttccataataaaaggctttgag 1246
 |||||||
 DB 166 AGGATGTGCCACTGGCAAAATGTAACTGTGCCAGTCTTTCCATAATAAAAGGCTTTGAG 107
 |||||||
 QY 1247 ttaactcactgaggggtatctgacaatgtgaggttatgaacaaagtggaggaatgaaat 1306
 |||||||
 DB 106 TTAACCTCACTGAGGTTTATCTGACAAATGCTGAGGTTATGACAAAGTGAGGAGATGAAT 47
 |||||||
 QY 1307 gtatgtgctcttagcaaaaaacatgtatgtgcatttcaatccacgt 1352
 |||||||
 DB 46 GTATGTGCTCTTTAGCAAAAAACATGTATGTGCATTTCAATCCCAAGT 1

Search completed: July 26, 2002, 17:57:13
 Job time: 12327 sec

[illegible]

called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the RRV genome sequence, and AAB53123 to AAB53204 represent the proteins encoded by the genome sequence. The present invention also specifically claims the individual open reading frame (ORF) nucleotide sequences from the genome which encode the individual proteins, but these sequences are not given. A non-human animal infected with RRV can be used for testing the efficacy of drug in the treatment of condition associated with infection with RRV such as Kaposi's sarcoma, lymphoproliferative disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly, hypergammaglobulinemia or autoimmune haemolytic anaemia, by administering the drug to an immuno-compromised non-human primate preferably Rhesus macaque monkey obtained by as a result of infection by Simian Immunodeficiency Virus (SIV). RRV is useful for producing non-human primate model for testing potential treatments for conditions associated with RRV infection. It is also useful for testing the efficacy of the candidate vaccine against RRV infection or conditions associated with its infection by administering the vaccine to the subject capable of infection with RRV, inoculating the subject with RRV and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205 to AAB53213 represent sequence used in the exemplification of the present invention.

Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;

Query Match 26.3%; Score 404.6; DB 21; Length 133719;
Best Local Similarity 66.9%; Pred. No. 1.7e-94;
Matches 575; Conservative 0; Mismatches 284; Indels 0; Gaps 0;

Qy 187 cacggggagctcagtaacctggggcagatccaacacatcctcgctcgggcgctcaggaag 246
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Db 21537 CACGGCCAGCTGCAGTACTTGGCCACCTGGATTATTAATTAACACGGCGGTCACAGG 21578
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[illegible][illegible]

Qy 367 ttgctgtggtttatcaaggatccacaatgtctaaagctgtcttccaaggagtga 426
|||||
Db 21457 ttgctgtggtttatcaggggtccaccgacttccacggactgtccggcgccgctaaa 21398

DQ 427 ATCTGGATGCCAATGATCCGAGACTTTTGGACAGCCTGGATTCTCCACCAGAAA 486

Db 21397 ATTGGACGGCACGGGTCCCGCCCTTTTGGCGGCGCAGGGCTTCGGGACCGCCGC 21338

[illegible]

Db 21277 GGGGCCGACGCCAATCAGGAGGGTCAGGGGTGGACCAAGCTGGCTTACGTGGTGGATCTA 21218

Db 21217 ATTAACAGGCGCCCCAGCATCGGCGCATCGTATGTCGCGTGGAAACCCCGGGGACTC 21158

Db 21157 GGCGGATGGCTCCCTCCTGTACAGTTTGTGTACGTTTACGTTTGCTCGGGGGGAG 21098

Db 21097 CTGTCTGTGCCAGTGTAACAGAGGTCCGCGACATGGGCTCCGGGGTCCCGTTTAAATC 21038

Db 21037 GCCAGTACGCCCTCCAGACGATCTGATCGTCACTACGGGCGCTACCCCGGGAGAC 20978

Qy	847	ttatcacacacttggagatgacataattttactcgtgaatcacatcgaccactcaaaatt	906
Db	20977	TTTGTGCACACCTTGGGTGACGCCCGCTTTACAAACACACGTGATCCCTGCTGCTT	20919
Qy	907	cagcttcagcgcgagaccagacacctttcccacaagctccaggattcttcgaaaaattgagaaa	966
Db	20917	CAGCTCGGAGGACCCCGCTCGCTTTCCGGCGCTGAAGATTTTGAGAAAGTGGCGCGT	20851
Qy	967	attgatgacttcaagctgaagacttccagattgaagagggtacaatccgatccaaactatt	1026
Db	20857	CTGGAGGACTTACCGCGCGGAGCTGAGTCTCGAGGGCTACGACCCCATCCCCACATA	20799
Qy	1027	aaaatgaaatggctgttt	1045
Db	20797	GAGATGGAGATGGCGGTTT	20779
RESULT	9		
AAV10240			
TD	AAV10240 standard; DNA; 1014 BP.		
AC	AAV10240;		
XX			
DT	15-JUL-1998 (first entry)		
XX			
DE	Human herpesvirus 8 (HHV-8) divergent locus DL-B probe 1.		
XX			
KW	DL-B; thymidylate synthase; dihydrofolate reductase; probe; HHV-8;		
KW	Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein;		
KW	Kaposi's sarcoma; beta-chemokine-like; hybridisation; VIL-6; ss.		
XX			
OS	Synthetic.		
OS	Kaposi's sarcoma associated herpesvirus.		
XX			
PN	W09804284-A1.		
XX			
PD	05-FEB-1998.		
XX			
PF	24-JUL-1997; 97WO-US12931.		
XX			
PR	25-JUL-1996; 96US-0022591.		
XX			
PA	(UYJO) UNIV JOHNS HOPKINS.		
XX			
PI	Hardwick JM, Hayward GS, Nicholas J, Reitz MR;		
XX			
DR	WPI; 1998-130422/12.		
PT	New human herpes virus gene region containing 8 open reading frames		
PT	useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based		
PT	large cell lymphoma		
XX			
PS	Claim 4; Pages 51-52; 84pp; English.		
XX			
CC	The present probe was synthesised for detecting human herpesvirus-8		
CC	(HHV-8) divergent locus DL-B which lies between open reading frames		
CC	11 and 17. Sequencing of the HHV-8 divergent locus DL-B revealed		
CC	the presence of nine viral ORFs with gene products related to cellular		
CC	proteins. These proteins include the thymidylate synthase (TS),		
CC	dihydrofolate reductase (DHFR), Bcl-2 homologue, IE-1A, IE-1B and,		
CC	four cytokines which include viral interleukin-6 (VIL-6), viral		
CC	macrophage inhibitory protein (VMP)-1A and -1B and beta-chemokine-like		
CC	(BCK) protein. The sequences of these proteins are given in		
CC	AAW0100-W40108. The invention claims the mentioned proteins and a		
CC	polynucleotide containing HHV-8 genes encoding one or more of these		
CC	proteins. The invention also claims that the polynucleotide and the		
CC	proteins may be used directly or indirectly, e.g. using antibodies to		
CC	the proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's		
CC	sarcoma, Castleman's disease, multiple myeloma and body cavity based		
CC	large cell lymphoma (BCBL). The proteins have also been claimed to be		
CC	useful in screening compounds for drugs to treat HHV-8 diseases.		
XX			
SQ	Sequence 1014 BP; 216 A; 239 C; 286 G; 273 T; 0 other;		

SQ Sequence 1014 BP; 216 A; 239 C; 286 G; 273 T; 0 other;

```

|||||
Db 181 aaatctgtccgtgacctatcagttattatttaagtgatgtgccactggcaaatgta 240
QY 1211 actgtgcagattttccataataaaaggctttgagtttaactcaactgagggtatctgaca 1270
Db 241 actgtgcagttttccataataaaaggctttgagtttaactcaactgagggtatctgaca 300
QY 1271 atgtcagggttatgaacaaagtggaggagaatgaaatgtatgtctcttagcaaaacatg 1330
Db 301 atgtcagggttatgaacaaagtggaggagaatgaaatgtatgtctcttagcaaaacatg 360
QY 1331 tatgtgatttccactccactactataaagaagggtgtgtgaatttcacaaagtatttt 1390
Db 361 tatgtgatttccactccactactataaagaagggtgtgtgaatttcacaaagtatttt 420
QY 1391 tggaaatattttagaatattttaaagaatttcaaaagctattccctcaaatgtaggagc 1450
Db 421 tggaaatattttagaatattttaaagaatttcaaaagctattccctcaaatgtaggagc 480
QY 1451 tgaataacacatcatgatgtaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1510
Db 481 tgaataacacatcatgatgtaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
QY 1511 tttgtctataataaagaagtgtctgc 1536
Db 541 tttgtctataataaagaagtgtctgc 566

RESULT 6
AAH74201
ID AAH74201 standard; DNA; 124884 BP.
XX
AC AAH74201;
XX
DT 15-OCT-2001 (first entry)
XX
DE Nucleotide sequence of the Varicella virus Dumas strain.
XX
KW Dumas strain; pox vaccine; vaccine; poxvirus disease; chickenpox; ss.
XX
OS Varicella virus.
XX
PN W0200156600-A1.
XX
PD 09-AUG-2001.
XX
PF 31-JAN-2001; 2001WO-JP00678.
XX
PR 31-JAN-2000; 2000JP-0062734.
XX
PA (OSAU ) UNIV OSAKA.
XX
PI Gomi Y, Sunamachi H, Takahashi M, Yamanishi K;
XX
DR WPI; 2001-48845/53.
XX
PT Method for checking absence of mutation at specific positions of
PT varicella virus genome for quality control of attenuated live varicella
PT vaccine -
XX
PS Claim 1; Page 61-105; 158pp; Japanese.
XX
CC The present sequence represents the nucleotide sequence of Varicella
CC virus, Dumas strain. The specification describes a method for the
CC quality control of an attenuated pox vaccine, characterised in that
CC the DNA sequence of specific parts of the viral genome in a sample is
CC determined and proved to be conserved rather than mutated in comparison
CC with the same parts of a reference viral genome. The method is useful
CC for quality control of vaccines for use in the prevention of poxvirus
CC diseases such as chickenpox.
XX
SQ Sequence 124884 BP; 33789 A; 29295 C; 28177 G; 33623 T; 0 other;

```

```

Query March 26.6%; Score 408; DB 22; Length 124884;
Best Local Similarity 66.5%; Pred. No. 2.1e-95;
Matches 585; Conservative 0; Mismatches 295; Indels 0; Gaps

QY 189 cggggaagctcagtaactcctggggagatccaaacacatcctcctcgtcggcgtaagaagga 248
Db 18488 cggggaacttcagttactaaacaaagtgatattttaaggtatggatctcgaaacg 1854
QY 249 cgaccgcagcggcgaccgcaccctctgggtattcggcatgcaggcgctacacacctgag 308
Db 18548 cgatcgaaacgggaatcggaacttatctttatttggaatgcaagctcgatacaattgog 1860
QY 309 agatgaattccctctcgtcgacaacccaacgtgtgttctgggaaggggtgtttggaggagtt 368
Db 18608 aaatgaattccctctttaaactacaagcgtgttttttgaggggcgctcgtgggaaggtt 1866
QY 369 gctgtgtttatacaaggatccacaataatgtaagagctgtcttccaaggaggagtaaaat 428
Db 18668 gttatgtttttatcggcggtcaacogattccaagaactcgccgttaagaataacacat 1872
QY 429 ctgggatgccaatggatcccgagactttttggacagcctgggattctccaccagagaaga 488
Db 18728 atgggatatacggatcgagacgaatttctaataatggaatggtcttccataaaagacac 1878
QY 489 aggggacttggcccgagtttatgcttccagtgaggcattttggggcgagaatacagaga 548
Db 18788 gggggacttggcccgatttaacagaaagtaacgtcagctgcaaaactgttagatacaat 1884
QY 549 tatggaatcagattattcaaggagggagttgacaaactgcaaaagtgattggtgacacat 608
Db 18848 ctgtcaatcaactatttacagaaagtaacgtcagctgcaaaactgttagatacaat 1890
QY 609 caaaaccaacccgtgacagacagagaatcatcatgtgcttggaaatccaagagatcttcc 668
Db 18908 taaacaaaccccgaaagcgacgaatgattatactgttggaaatccaagagatcttcc 1896
QY 669 tctgtgctgctgcctccatgcctcctgcctcctgccttctatgtgtggaacagtggct 728
Db 18968 cttaatggtactacctccatgctcacacgttatgtcagttttacgttgcaaacggtgaatt 1902
QY 729 gtctgcagctgtacacagatcgaggagacatgggagcattgggctcgttcttcaacatcgc 788
Db 19028 atctgcgaagtataccagagatcggggagatgggcttggggtacgttcaacatcgc 1908
QY 789 cagetaagcctgctcacgtacatgatgctgcacatcacggcctgaagccaggtgactt 848
Db 19088 tggatagtcactcttaccctacatagtagcgacatggttacaggacttaaaacccgagatt 1914
QY 849 tatcacacactttggagatgcacatatttacctgaatcacatcgagccactgaaattcca 908
Db 19148 aattcacaatgggggagtgacatatttaccttgaatcatatagatgctttaaagtcca 1920
QY 909 gcttcagcggaacccagacccttccaaagctcaggtattcttcgaaagtgtgagaaat 968
Db 19208 gctagctgactcccaaaaccccttcccttgccttaaaattattcgaattgaacagatcat 1926
QY 969 tgaatgactcaaaagctgaagactttcagattggaaggtgacaaatccgcacatcccaactataa 1028
Db 19268 aaacgactttaaatgggagcaggttttcagcttgatggatataataatccacccccccctaaa 1932
QY 1029 aatggaatggctgttttggtgcttttcaaaaggagctcga 1068
Db 19328 aatggaatggctgttttggtgcttttcaaaaggagctcga 19367

RESULT 7
AAH74202
ID AAH74202 standard; DNA; 125157 BP.
XX
AC AAH74202;
XX
DT 15-OCT-2001 (first entry)

```



```
QY 1530 gtctgc 1536
DB 99 GTCTGC 93

RESULT 3
AAF31109
ID AAF31109 standard; CDNA; 18596 BP.
AC AAF31109;
XX
XX
XX 27-APR-2001 (first entry)
XX
XX Thymidylate synthase coding sequence.
DE
XX
XX Analyte-binding enzyme; analyte analysis; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200102600-A2.
PN
XX
XX 11-JAN-2001.
PD
XX
XX 30-JUN-2000; 2000WO-US18057.
PF
XX
XX 06-JUL-1999; 99US-0347878.
PR
XX 06-DEC-1999; 99US-0457205.
FR
XX
XX (GEAT ) GEN ATOMICS.
PA
XX
XX Yuan C;
PI
XX
XX WPI; 2001-071583/08.
DR
XX
XX Assaying method, useful for prognosis and diagnosis of disease,
PT comprises contacting sample with a mutant analyte-binding enzyme and
PT detecting binding -
XX
XX Disclosure; Page -: 187pp; English.
XX
XX The present invention relates to a method for assaying an analyte in a
CC sample comprising: contacting the sample with a mutant analyte-binding
CC enzyme which has binding affinity for the analyte or an immediate
CC analyte enzymatic conversion product but has attenuated catalytic
CC activity; and detecting resulting binding. The method is useful in
CC monitoring biological systems/processes, or prognosis/diagnosis of
CC disease caused by imbalances of the analytes. The present sequence is
CC a coding sequence used in the present invention.
CC Note: the present sequence is not shown in the specification, but was
CC from Genbank, using information given in the specification.
XX
XX Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
SQ

Query Match 39.9%; Score 613.2; DB 22; Length 18596;
Best Local Similarity 90.6%; Pred. No. 2e-149;
Matches 667; Conservative 0; Mismatches 63; Indels 6; Gaps 1;

QY 807 gtacatgattgcgcacatcacggcgccctgaagccagggtgactttatcacacactttgggaga 866
DB 15510 gaactttgtgatacacctctgtactgttttcacggacatgaggagcaattacaacag 15569

QY 867 tgcacattattacctgaatcacatcgacatgcacatgaaattcagcttcagcgagaaacccag 926
DB 15570 gtcgtacaattatggcaaaataatggccttattgttttagcttcagcgagaaacccag 15629

QY 927 acctttcccaagctcaggattcttcgaaaagttagaaattgatgacttcaaaactga 986
DB 15630 acctttcccaagctcaggattcttcgaaaagttagaaattgatgacttcaaaactga 15689

QY 987 agactttcagattgaagggtacatccgactccaacttaaaatgaaatgactgttta 1046
DB 15690 agactttcagattgaagggtacatccgactccaacttaaaatgaaatgactgttta 15749
QY 1047 gggtgctttcaaaagagactCgaagatattgtcagttcagtttgagggttgaggctgagcg 1106
DB 15750 gggtgctttcaaaagagactCgaagatattgtcagttcagtttgagggttgaggctgagcg 15809
QY 1107 agtataaagtctcttttctctctctctctctctctctctctctctctctctctctctctct 1166
DB 15810 agtataaagtctcttttctctctctctctctctctctctctctctctctctctctctctct 15869
QY 1167 ctatcagttatttaatttttaaggatgttgcactggcaaaatgaactgtccagttcttt 1226
DB 15870 ctatcagttatttaatttttaaggatgttgcactggcaaaatgaactgtccagttcttt 15929
QY 1227 ccataataaagccttttgagtttaactcaactgaggggtatctgacaatgctgaggttatgaa 1286
DB 15930 ccataataaagccttttgagtttaactcaactgaggggtatctgacaatgctgaggttatgaa 15989
QY 1287 caaagtgaaggagaatgaatgtatgtctctctctctctctctctctctctctctctctctct 1346
DB 15990 caaagtgaaggagaatgaatgtatgtctctctctctctctctctctctctctctctctctct 16049
QY 1347 ccacgtactataaagaaggttggaattcaacagctatttttgaattatttttagaa 1406
DB 16050 ccacgtactataaagaaggttggaattcaacagctatttttgaattatttttagaa 16109
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DB 16110 tattttaagaatttccaaagctattccctcaaatctgagggagctgagtaacacatcga 16169
QY 1467 tcatgatgtagagtggtttatgaactttaA-----agttgttttatatgttgctataa 1520
DB 16170 tcatgatgtagagtggtttatgaactttaA-----agttgttttatatgttgctataa 16229
QY 1521 taaagaagtgtttctgc 1536
DB 16230 taaagaagtgtttctgc 16245

RESULT 4
AAC91215
ID AAC91215 standard; DNA; 18596 BP.
XX
AC AAC91215;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human thymidylate synthase gene SEQ ID NO: 11.
XX
KW Human; schizophrenia; developmental disorder; spina bifida cystica;
KW Tourette's syndrome; bipolar illness; autism; conduct disorder;
KW attention deficit disorder; obsessive compulsive disorder;
KW chronic multiple tic syndrome; learning disorder; polymorphism; ds.
XX
OS Homo sapiens.
XX
XX WO200071754-A1.
XX
XX 30-NOV-2000.
XX
XX 24-MAY-2000; 2000WO-US14354.
XX
XX 25-MAY-1999; 99US-0318448.
XX
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
XX Johnson WG, Stenroos ES;
XX
XX WPI; 2001-025174/03.
XX
XX Diagnosing a developmental disorder, e.g. schizophrenia, by forming
PT datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
PT and environmental variables affecting an individual and then comparing
```


TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1292 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-283-471A-37

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	Best Local Similarity	54.1%;	Pred. No. 0.002;		
	Matches	99;	Conservative	0;	Mismatches 84; Indels 0; Gaps
QY	10	ggagacaattggtcgtgccttcctccgcgcgcgaacttgacctgctcgctccgccgcgcg	69		
Ddb	443	GGACCCCAACCGCCGCGTGGGCCCGGGGGCGGGGCTGACCCCTCCACCACCCCCCTCG	502		
QY	70	ceatttgcctgcctccgtcccccccgcgcgcgcacatgectgtggccgggtctcgagactg	129		
Ddb	503	CGCCCTTCGCGCTTCGCGCGGCCTCGCCCTCGCGCTCGCGGTACGCGGGAGCACTG	562		
QY	130	cgcgcgcgcgcctttgccccccgcgcgcacagagcgcgcgcgcgcgcgcgcgcgcac	189		
Ddb	563	GCGCGCTGCGCCTTGCGACCGCGGGCGGGAGGGGGCGCCGGAGCCCCCGCGCAACCCC	622		
QY	190	ggg	192		
Ddb	623	GCG	625		

RESULT 15
 : Sequence 3, Application US/08458568A
 : Patent No. 5821339
 : GENERAL INFORMATION:
 : APPLICANT: Schaifer, Priscilla A.
 : APPLICANT: Yeh, Lily
 : TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvir
 : TITLE OF INVENTION: Infections
 : NUMBER OF SEQUENCES: 15
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
 : STREET: One Liberty Place, 46th floor
 : CITY: Philadelphia
 : STATE: PA
 : COUNTRY: USA
 : ZIP: 19103
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Wordperfect 5.1
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/458,568A
 : FILING DATE: 02-JUNE-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/065,146
 : FILING DATE: 05-MAY-1993
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Leary Ph.D., Kathryn R.
 : REGISTRATION NUMBER: 36,317
 : REFERENCE/DOCKET NUMBER: DFCI-0029
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (215) 568-3100
 : TELEFAX: (215) 568-3439
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 702 base pairs

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;
US-09-089-195-1

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Query Match          99.7%; Score 1531.2; DB 3; Length 1536;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1533; Conservative 0; Mismatches 3; Indels 0;
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05

[illegible]

QY 961 gagaaatgatgcctcaagcgtcaaacctttcaagatgaaggtcaaatccgcatcca 1020

Db 961 GAGAAAATGATGACCTTCAAGAGTCGAGACTTTCGATGAGAGGTACAATCCGATCCA 1020

QY 1021 actattaaatgaaatggctgtttagggtgctttcaagaggctCgaagatattgtca 1080

Db 1021 ACTATTAATAATGAAATGGCTGTTTAGGGTGCTTTCAAGAGCTTGAAGATATTGTCA 1080

QY 1081 gtcttaggggttgggctgagatccagaggtaaaaagttctctttgtctataaacaagaag 1140

Db 1081 GTCCTTAGGGGTGGGCTGGATCCGAGGTAAAAGTTCCTTTTGCTCTAAAAGAAAAGG 1140

QY 1141 aactcagctcaaaaactctgcgtgaacctacagttatttaatttcaaggatgttgcact 1200

Db 1141 AACTAGGTCAAAAATCTGCTCGTACCTATACAGTATTAAATTTTAAGGATGTGCAC 1200

QY 1201 ggcataatgaactgtgccagttctttccataataaaaagcgttgagtttaactcaactgagg 1260

Db 1201 GGCAAAATGTAACGTGCCAGTCTTTCCATAATAAAAAGGCTTGAGTTAACTCAGTSGG 1260

QY 1261 gtactgacaatgtcgaagttatgaacaagtggaggagaatgaatgtatgtctcttaag 1320

Db 1261 GTATCTGACAATGCTGAGGTTATGACAAAGTGAGGAGATGAATGATGTGCTCTTAG 1320

QY 1321 caaaaacatgtatgtgaattccaatccacagctacttataaagaaggttgggtgaattcac 1380

Db 1321 CAAAACATGATGTATGTCATTTCAATCCACGACTATTAAAGAAGGTTGGTGAATTCAC 1380

QY 1381 aagctattttgtgaaatatitttagaataatttaagaattccaagctattccctcaaat 1440

Db 1381 AAGCTATTTTGGAAATATTTTAGAATAATTTAAAGAATTTCAAGCTATTTCCTCAAA 1440

QY 1441 ctgaggagactgagttaacacatcgatcatatgatatagatgttggttgaacttaagct 1500

Db 1441 CTGAGGAGCTGAGTAACACCATCGATCATGATGTAGAGTGGTATGACTTTATGT 1500

QY 1501 tgttttatgtgtcataataaagaagttcttcgc 1536

Db 1501 TGTTTTATGTGTGTATAATAAAGAAGTGTCTGCG 1536

RESULT 2

US-09-318-448-11

US-09-318-448-11, Application US/09318448

Patent No. 6210950

GENERAL INFORMATION:

APPLICANT: Johnson, William G.

APPLICANT: Stentcos, Edward S.

TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING

TITLE OF INVENTION: DEVELOPMENTAL DISORDERS

FILE REFERENCE: 601-1-057

CURRENT APPLICATION NUMBER: US/09/318,448

CURRENT FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 11

LENGTH: 18596

TYPE: DNA

ORGANISM: Homo sapiens

US-09-318-448-11

[illegible]

[illegible]

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CDS
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/EC_number="2.1.1.45"
/codon_start=1
/product="thymidylate synthase"

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Query Match

18596 bp DNA linear PAT 08-AUG-2000
rom patent US 6210950.
EI:15106832
O 18596)
and Stenroos, E.Scott.
to a combination of genetic and environmental factors
to diagnosing, preventing, and treating developmental
0950-A 11 03-APR 2001;
tion/Qualifiers
18596
anism="unknown"
991 C 4479 g 5605 t
98.0%: Score 1163.8: DB 6: Length 18596:

PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234937.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246528.
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PR 08-NOV-2000; 2000US-0246609.
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PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249269.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.

PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
FI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
FT metastasis -
XX
XX Disclosure; SEQ ID NO 36572; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK34942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 56743 BP; 14298 A; 13270 C; 14240 G; 14935 T; 0 other;

Query Match 17.2%; Score 204.2; DB 22; Length 56743;
Best Local Similarity 71.3%; Pred. No. 1.2e-36;
Matches 320; Conservative 0; Mismatches 105; Indels 24; Gaps 3

QY 1 gatcgccactgcaactcagctgggtgagagcagcagactgtctctcaaaaaaaa 60
Db 1834 gattgcacactgcaactcagctgggtgagagcagcagactgtctctcaaaaaaaa 1893
QY 61 aaaaagaccgccagggtctcaaaacaaacacctcggaacccctggcggtctttttt 120
Db 1894 taataatgaaacactcagtgcagatactggccttaggttttct----ttcttttc 1949
QY 121 ttt 180
Db 1950 ttt 2009
QY 181 cggatcttggtcactgcaactcgtcctcccaggttccaagaattcttctgcctcagcc 240
Db 2010 gtgatctcgtcactgcaactcgtcctcccaggttccaagaattcttctgcctcagcc 2069
QY 241 tcccaagtag-----ccacacagccacagtaatttttgtanttta 281
Db 2070 tcccgagtagctggaattcacaggcgccccacacatgcgcgctaatttttgtanttta 2129
QY 282 gttagagcggggttttcccatgtgtccaggctgtgtcngaatcctgcactcaggtga 341
Db 2130 gcagagac-ggggttttctcctgttggcagggtgtgtcngaatcctgcactcaggtga 2188

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23014.
XX Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
OS W0200157182-A2.
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US01354.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225287.
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XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
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XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0222081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
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XX 14-SEP-2000; 2000US-0232401.
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XX 14-SEP-2000; 2000US-0233064.
XX 14-SEP-2000; 2000US-0233065.
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PR 21-SEP-2000; 2000US-0234274.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
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PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
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PR 17-NOV-2000; 2000US-0249244.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
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PR 17-NOV-2000; 2000US-0249299.
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PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.

CC activity, and can be used in gene therapy and vaccine production. (1)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 11553 BP; 3513 A; 2418 C; 2597 G; 3025 T; 0 other;

Query Match 17.2%; Score 204.6; DB 22; Length 11553;
 Best Local Similarity 72.0%; Pred. No. 9.8e-27;
 Matches 316; Conservative 0; Mismatches 101; Indels 22; Gaps 3;
 QY 1 gatcgccactgcactccagcctgggtgagagagagactctgtctcaaaaaa 60
 DB 8023 GATCGCGCCACCGCACTCCAGCCTGGCGGACAGACTGACACTCCGCTCAAAAAATAA 7964
 QY 61 aaaaagaccgcgggtcacaacaa--aaacctcggaagacctgcggtcttttt 118
 DB 7963 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 7904
 QY 119 ttt 178
 DB 7903 CTTTTTTTTTTTTTTTTTTTGTAGACAGGGCTGTGCTGTGCTGCTGCTGCTGCTGCTG 7844
 QY 179 gtcgatctgtgctcactgcacactctgcctccaggttccagcaattcttcgctcag 238
 DB 7843 GTGCGATCTGACCTCACTGCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7784
 QY 239 cctcccaagtag-----caccacgcccagcactaattttgtanttt 279
 DB 7783 TCTCTGTAATAGCTGGGATATACAGATGTGCACACACACACACACACACACACACACACAC 7724
 QY 280 tagtagacaggggtttccaccatgttgcaggtggtctngaaactcctgacctcag 339
 DB 7723 TAGTAGAGA-TGGGGTTTGGCCATGTTGGCCAGGCTGTTTGAACCTCCAGACTCAAGT 7665
 QY 340 gatccacccgctcggcccccacaaagtagtagattacaggtgagccacccgctccag 399
 DB 7664 GATTGCTCCCTTGGCCTCCCAAGTCTGGGATACAGGCTGAGCCACACACACACACACAC 7605
 QY 400 cgcctcggcggttttaatt 418
 DB 7604 CCAACAATCAGCTTGATT 7586

RESULT 10

AAK66874/C

ID AAK66874 standard; DNA; 37449 BP.

XX

AC AAK66874;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21686.

XX

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX

KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX

OS Homo sapiens.

XX

FN WO200157182-A2.

XX

PD 09-AUG-2001.
 XX 17-JAN-2001; 2001WO-US01354.
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
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 PR 07-JUN-2000; 2000US-0209457.
 PR 28-JUN-2000; 2000US-0214886.
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 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
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 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
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 PR 01-SEP-2000; 2000US-0229287.
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 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
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 PR 14-SEP-2000; 2000US-0232399.
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 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.

CC Cancers and cancer metastases of haematopoietic-derived cells, especially
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK8211
XX represent sequences used in the exemplification of the present invention
SQ Sequence 11453 BP; 3521 A; 2392 C; 2561 G; 2979 T; 0 other;

Query Match 17.2%; Score 204.6; DB 22; Length 11453;
Best Local Similarity 72.0%; Pred. No. 9.8e-27;
Matches 316; Conservative 0; Mismatches 101; Indels 22; Gaps

QY 1 gatcgccactgacccagctggtgagagagcagactctgtctcaaaaaa 60
Db 7923 GATCGCGCCACCGCCTCCAGCTGGCGCAGACTCCGTCCTCAAAAAATAA 7864
QY 61 aaaaagaccgcccagggctcaaaaaa--aaacctcggaagccctggcggtcttttt 118
Db 7863 AATAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 7804
QY 119 ttt 178
Db 7803 CTT 7744
QY 179 gtccgattgtgctcaactgcaacctgtctccaggttccaggaattcttctgcctcag 238
Db 7743 GTCCGATCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 7684
QY 239 cctcccaagtag-----ccaccagccagcctaattttgtanttt 279
Db 7683 TCTCTGAATAGCTGGGATACAGATGTCACACCCACCCGCGCTAATTTTGCATTTT 7624
QY 280 tagtagagacgggggtttccaccatgttgcaggtgtctncaactctgacctcaggt 339
Db 7623 TAGTAGAGA-TGGGGTTTGGCATGTGGCCAGGCTGGTTTGAATCCAGACCTCAAGT 7565
QY 340 gatccaccgctcctggcccccacaaagtagtagattacaggtgagccacgcgcgcag 399
Db 7564 GATTGTCTCCCTTGGCCCTCCAAAAGTCTGGGATTACAGCGCTGAGCCACGCCCGG 7505
QY 400 cgcctggcggttttaatt 418
Db 7504 CCAACAATCAGCTTTGATT 7486

RESULT 9
AAK73271/c
ID AAK73271 standard; DNA; 11553 BP.
XX AC AAK73271;
XX AC AAK73271;
DT 06-NOV-2001 (first entry)
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28083.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW Cytostatic; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.
XX PN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180528.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.

PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
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PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246529.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249208.
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PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
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PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX Disclosure; SEQ ID NO 28084; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
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XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
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 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
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 PR 08-NOV-2000; 2000US-0246610.
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 PR 17-NOV-2000; 2000US-0249207.
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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 20393; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK67694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAK62169 represent sequences used in the exemplification of the present invention.

Sequence 56632 BP; 17016 A; 8910 C; 10552 G; 20154 T; 0 other;

XX Disclosure; Page -: 187pp; English.
 PS The present invention relates to a method for assaying an analyte in a
 CC sample comprising: contacting the sample with a mutant analyte-binding
 CC enzyme which has binding affinity for the analyte or an immediate
 CC analyte enzymatic conversion product but has attenuated catalytic
 CC activity; and detecting resulting binding. The method is useful in
 CC monitoring biological systems/processes, or prognosis/diagnosis of
 CC disease caused by imbalances of the analytes. The present sequence is
 CC a coding sequence used in the present invention.
 CC Note: The present sequence is not shown in the specification, but was
 CC from Genbank, using information given in the specification.
 XX
 SQ Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;

Query Match 98.0%; Score 1163.8; DB 22; Length 18596;
 Best Local Similarity 99.1%; Pred. No. 8.6e-192;
 Matches 1176; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 gatcgccactgactccagctgggtgagagcgagactctgtctcaaaaaa 60
 Db 78 gatcgccactgactccagctgggtgagagcgagactctgtctcaaaaaa 137
 QY 61 aaaaagacccagggctcaaaaaaacctcgaaaagccctggcgtctttttt 120
 Db 138 aaaaagacccagggctcaaaaaaacctcgaaaagccctggcgtctttttt 197
 QY 121 ttt 180
 Db 198 ttt 257
 QY 181 cggatttggctcaactgcaactctgctccaggttcaagcaattcttgcctcagc 240
 Db 258 cggatttggctcaactgcaactctgctccaggttcaagcaattcttgcctcagc 317
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 Db 318 tcccaagtgcacacacccagcttaatttttttttttttttttttttttttt 377
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 Db 378 catgtgtccaggtggtcttngaaactctgactcaggtgacccagctcgccccc 437
 QY 361 caaagtactagattacaggtgagccacccgctccagccctggcgttttttaatca 420
 Db 438 caaagtactagattacaggtgagccacccgctccagccctggcgttttttaatca 497
 QY 421 agtagaaagctgcaattatacacttcttcttcttcttcttcttcttcttcttct 480
 Db 498 agtagaaagctgcaattatacacttcttcttcttcttcttcttcttcttcttct 556
 QY 481 aaatgcaaatAacttattagtttagaaacagatctcaaacacagcttttngacaag 540
 Db 557 aaatgcaaatccctattagtttagaaacagatctcaaacacagcttttngacaag 616
 QY 541 accgcaggaacacgtggaaactgtgctggttagaagagcgctgcacagacgg 600
 Db 617 accgcaggaacacgtggaaactgtgctggttagaagagcgctgcacagacgg 676
 QY 601 ttcccaaaagggcagctctccnccgacccgcaactgntccaggttcccggtttcct 660
 Db 677 ttcccaaaagggcagctctccnccgacccgcaactgntccaggttcccggtttcct 736
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 Db 737 aagactctcagctgtggccctggcgtcttctgtgtgcaaccccgctgctcgttttc 796
 QY 721 cccttgccagcgtctcttagagcggggcccgcgcgcgcgcgcgcgcgcgcgcgcgc 780
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RESULT 2

AAC91215
 ID AAC91215 standard; DNA; 18596 BP.

XX AC AAC91215;
 XX DT 20-MAR-2001 (first entry)
 XX Human thymidylate synthase gene SEQ ID NO: 11.
 DE Human; schizophrenia; developmental disorder; spina bifida cystica;
 KW Tourette's syndrome; bipolar illness; autism; conduct disorder;
 KW attention deficit disorder; obsessive compulsive disorder;
 KW chronic multiple tic syndrome; learning disorder; polymorphism; ds.

XX OS Homo sapiens.
 XX PN WO200071754-A1.
 XX PD 30-NOV-2000.
 XX PF 24-MAY-2000; 2000WO-US14354.
 XX PR 25-MAY-1999; 99US-0318448.
 XX PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 XX PI Johnson WG, Stenroos BS;
 XX DR WPI; 2001-025174/03.
 XX PT Diagnosing a developmental disorder, e.g. schizophrenia, by forming
 PT datasets (DS) of genetic (e.g. genotypes of isolate metabolism alleles)
 PT and environmental variables affecting an individual and then comparing
 these DS with reference DS -

XX Disclosure; Page 125-131; 156pp; English.

CC The present invention provides a novel method of estimating the
 CC susceptibility of an individual to a developmental disorder using genetic
 CC and environmental variables. The method can be used in the diagnosis,
 CC prevention and treatment of disorders such as schizophrenia, spina bifida
 CC cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
 CC attention deficit disorder, obsessive compulsive disorder, chronic

Db 184 GTACTGGGGCAGATCCAAACATCTCCGTGCGCGCTAGAGAGGACGACGCGG 243

QY 1080 caccggaacctgtcggtatttcggcatgcaggcgctacagcctgagagtga 1133
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Db 244 CACCGGCACCCCTGTCGTTATCGGCATGCAGCGCGCTACAGCCTGAGAGATGA 297
|||||

RESULT 14
AL542409 935 bp mRNA linear EST 16-FEB-2001
LOCUS AL542409 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE010YH04 5 prime
DEFINITION / mRNA sequence.
ACCESSION AL542409
VERSION AL542409.1 GI:12874425
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Pollayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CS0DE010YH04"
/clone.lib="LTI_FL002_P11"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 208 a 279 c 254 g 190 t 4 others
ORIGIN

Query Match 23.6%; Score 280.2; DB 9; Length 935;
Best Local Similarity 98.28; Pred. No. 1.5e-24;
Matches 280; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 849 cgtccgcgcgcgcacttggcgtcctccgtcccccgcgcgcacttgcgtcctccgtc 908
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Db 1 CGTCCCGCCGCGGCATTGGCGCTGCTCCGTCGCCGCGGCCTTGCCTGCTCGCTC 60
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QY 909 cccgcgcgcgcgcgcacttgcgttgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 968
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Db 61 CCGCGCCGCGCGCGCATGTCCTGTGCGCGCTCGGAGTGCAGCGCGCGCTTGCCTCC 120
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QY 969 cgcgcacagagcgggacgc 1028
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Db 121 CGCCGCACAGACGGGACGCGGAGCGCGCTCGCGCGCGCGGAGCTGCAGTACTGGG 180
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QY 1029 gcagatccacacatcctccgtcgtcggttcgagtgctgcgcgcgcgcgcgcgcgcgcgc 1088
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Db 181 GCAGATCCACACATCCTCCGCTGCGGGGTGTCAGGAGGACACCGCACCGGACCGGCAC 240
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QY 1089 cctgtcggtattcggcatggaaggcgctacagcctgagagtga 1133
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Db 241 CCTGTGCGTATTGCGCATGAGCGCGCTACAGCCTGAGARATGA 285
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